

RAW SEQUENCE LISTING

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Application Serial Number: 10/537, 201A
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DATE: 03/06/2006

PATENT APPLICATION: US/10/537,201A

TIME: 15:23:31

Input Set : A:\Seq. Listing. 2002-744US.txt

Output Set: N:\CRF4\03062006\J537201A.raw

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3 <110> APPLICANT: Van der Geize, Robert
4     Hessels, Gerda
5     Dijkhuizen, Lubbert
6     Van der Meijden, Peter
8 <120> TITLE OF INVENTION: New expression system from Rhodococcus
10 <130> FILE REFERENCE: 2002.744US
12 <140> CURRENT APPLICATION NUMBER: 10/537,201A
13 <141> CURRENT FILING DATE: 2005-06-02
15 <150> PRIOR APPLICATION NUMBER: PCT/EP03/050928
16 <151> PRIOR FILING DATE: 2003-12-02
18 <150> PRIOR APPLICATION NUMBER: EP02080054.6
19 <151> PRIOR FILING DATE: 2002-12-03
21 <160> NUMBER OF SEQ ID NOS: 13
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1543
27 <212> TYPE: DNA
28 <213> ORGANISM: Rhodococcus erythropolis
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(1533)
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37   1           5           10           15
39 ggc gga gcg ctg acc ggc gca tat acc gcc gct gct cag gga ttg acg   96
40 Gly Gly Ala Leu Thr Gly Ala Tyr Thr Ala Ala Ala Gln Gly Leu Thr
41           20           25           30
43 acg atc gtc ctc gag aaa acc gat cgt ttc ggc ggg acc tcc gcc tac   144
44 Thr Ile Val Leu Glu Lys Thr Asp Arg Phe Gly Gly Thr Ser Ala Tyr
45           35           40           45
47 tcg ggc gcc tcg atc tgg ctc cca ggt acc cag gtg cag gaa cgc gcc   192
48 Ser Gly Ala Ser Ile Trp Leu Pro Gly Thr Gln Val Gln Glu Arg Ala
49           50           55           60
51 gga ctt ccc gac tcg acc gag aat gcc cgc acc tat ctg cgc gcg ttg   240
52 Gly Leu Pro Asp Ser Thr Glu Asn Ala Arg Thr Tyr Leu Arg Ala Leu
53   65           70           75           80
55 ctc ggt gac gcc gag tcc gag cgc cag gac gcc tac gtc gag acc gct   288
56 Leu Gly Asp Ala Glu Ser Glu Arg Gln Asp Ala Tyr Val Glu Thr Ala
57           85           90           95
59 ccc gct gtc gtc gct cta ctc gag cag aac ccg aac atc gaa ttc gag   336
60 Pro Ala Val Val Ala Leu Leu Glu Gln Asn Pro Asn Ile Glu Phe Glu
61           100           105           110

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63	ttc	cgt	gcg	ttc	ccc	gac	tac	tac	aaa	gcc	gaa	ggc	cgg	atg	gac	acg	384
64	Phe	Arg	Ala	Phe	Pro	Asp	Tyr	Tyr	Lys	Ala	Glu	Gly	Arg	Met	Asp	Thr	
65			115						120				125				
67	gga	cgc	tcc	atc	aac	cct	ctc	gat	ctc	gat	ccc	gcc	gac	atc	ggg	gac	432
68	Gly	Arg	Ser	Ile	Asn	Pro	Leu	Asp	Leu	Asp	Pro	Ala	Asp	Ile	Gly	Asp	
69			130						135				140				
71	ctc	gcc	ggc	aag	gtg	cgt	ccg	gaa	ctg	gac	caa	gac	cgc	acc	ggg	cag	480
72	Leu	Ala	Gly	Lys	Val	Arg	Pro	Glu	Leu	Asp	Gln	Asp	Arg	Thr	Gly	Gln	
73	145								150				155			160	
75	gat	cat	gct	ccc	ggc	ccg	atg	atc	ggg	ggg	cgc	gca	ctg	atc	ggc	cgt	528
76	Asp	His	Ala	Pro	Gly	Pro	Met	Ile	Gly	Gly	Arg	Ala	Leu	Ile	Gly	Arg	
77					165					170					175		
79	ctg	ctg	gcc	gca	gtt	cag	agc	acc	ggg	aag	gca	gaa	ctt	cgc	acc	gaa	576
80	Leu	Leu	Ala	Ala	Val	Gln	Ser	Thr	Gly	Lys	Ala	Glu	Leu	Arg	Thr	Glu	
81					180					185					190		
83	tcc	gtc	ctc	acc	tcc	ctg	atc	gtg	gaa	gac	ggc	cgt	gtt	gtc	ggc	gcc	624
84	Ser	Val	Leu	Thr	Ser	Leu	Ile	Val	Glu	Asp	Gly	Arg	Val	Val	Gly	Ala	
85					195					200					205		
87	gag	gtc	gaa	tcc	ggc	ggc	gaa	acc	cag	cga	atc	aag	gcg	aac	cgc	ggg	672
88	Glu	Val	Glu	Ser	Gly	Gly	Glu	Thr	Gln	Arg	Ile	Lys	Ala	Asn	Arg	Gly	
89			210						215				220				
91	gtc	ctg	atg	gca	gca	ggc	ggc	atc	gaa	ggc	aac	gcc	gag	atg	cgt	gag	720
92	Val	Leu	Met	Ala	Ala	Gly	Gly	Ile	Glu	Gly	Asn	Ala	Glu	Met	Arg	Glu	
93	225					230					235				240		
95	cag	gca	ggc	acc	ccc	ggc	aag	gcg	atc	tgg	agt	atg	ggg	ccc	ttc	ggc	768
96	Gln	Ala	Gly	Thr	Pro	Gly	Lys	Ala	Ile	Trp	Ser	Met	Gly	Pro	Phe	Gly	
97					245					250					255		
99	gcc	aac	acc	ggc	gac	gcg	atc	tct	gcc	ggg	att	gct	gtc	ggc	ggc	gca	816
100	Ala	Asn	Thr	Gly	Asp	Ala	Ile	Ser	Ala	Gly	Ile	Ala	Val	Gly	Gly	Ala	
101					260					265					270		
103	aca	gcc	ttg	ctc	gat	cag	gcg	tgg	ttc	tgc	ccc	ggc	gtc	gag	cag	ccc	864
104	Thr	Ala	Leu	Leu	Asp	Gln	Ala	Trp	Phe	Cys	Pro	Gly	Val	Glu	Gln	Pro	
105					275					280					285		
107	gac	ggc	agc	gcc	gcc	ttc	atg	gtc	ggc	gtt	cgc	ggg	ggg	ctc	gtc	gtc	912
108	Asp	Gly	Ser	Ala	Ala	Phe	Met	Val	Gly	Val	Arg	Gly	Gly	Leu	Val	Val	
109			290						295				300				
111	gac	agc	gcc	ggg	gag	cgc	tac	ctc	aac	gag	tcg	ctt	ccg	tac	gac	cag	960
112	Asp	Ser	Ala	Gly	Glu	Arg	Tyr	Leu	Asn	Glu	Ser	Leu	Pro	Tyr	Asp	Gln	
113	305					310					315				320		
115	ttc	gga	cga	gcc	atg	gat	gct	cac	gac	gac	aac	ggg	tct	gcc	gtg	ccg	1008
116	Phe	Gly	Arg	Ala	Met	Asp	Ala	His	Asp	Asp	Asn	Gly	Ser	Ala	Val	Pro	
117					325					330					335		
119	tcg	ttc	atg	atc	ttc	gac	tcg	cgc	gag	ggg	ggc	gga	ctg	ccc	gcc	atc	1056
120	Ser	Phe	Met	Ile	Phe	Asp	Ser	Arg	Glu	Gly	Gly	Gly	Leu	Pro	Ala	Ile	
121					340					345					350		
123	tgc	atc	ccg	aac	acg	gcg	ccc	gcc	aag	cac	ctc	gaa	gcc	gga	acg	tgg	1104
124	Cys	Ile	Pro	Asn	Thr	Ala	Pro	Ala	Lys	His	Leu	Glu	Ala	Gly	Thr	Trp	
125					355					360					365		
127	gtc	ggg	gcc	gac	act	ctc	gaa	gaa	ctc	gct	gcc	aag	acc	gga	cta	ccg	1152

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128 Val Gly Ala Asp Thr Leu Glu Glu Leu Ala Ala Lys Thr Gly Leu Pro
129      370      375      380
131 gcc gac gca ttg cgc agc act gtc gaa aag ttc aac gat gcc gca aaa 1200
132 Ala Asp Ala Leu Arg Ser Thr Val Glu Lys Phe Asn Asp Ala Ala Lys
133 385      390      395      400
135 ctg ggc gtc gac gaa gag ttc cat cgc ggc gaa gac ccg tac gac gcg 1248
136 Leu Gly Val Asp Glu Glu Phe His Arg Gly Glu Asp Pro Tyr Asp Ala
137      405      410      415
139 ttc ttc tgc cca ccc aac ggc ggt gcg aat gcg gca ctg acg gcc atc 1296
140 Phe Phe Cys Pro Pro Asn Gly Gly Ala Asn Ala Ala Leu Thr Ala Ile
141      420      425      430
143 gag aac gga ccg ttc tac gcg gcc cgc atc gtc ctc agt gac ctc ggc 1344
144 Glu Asn Gly Pro Phe Tyr Ala Ala Arg Ile Val Leu Ser Asp Leu Gly
145      435      440      445
147 acc aag ggc gga ttg gtc acc gac gtc aac ggc cga gtc ctg cgt gct 1392
148 Thr Lys Gly Gly Leu Val Thr Asp Val Asn Gly Arg Val Leu Arg Ala
149      450      455      460
151 gac ggc agc gcc atc gac ggc ctg tac gcc gcc ggc aac acg agc gcg 1440
152 Asp Gly Ser Ala Ile Asp Gly Leu Tyr Ala Ala Gly Asn Thr Ser Ala
153 465      470      475      480
155 tca ctg agc ggc cgc ttc tac ccc ggc ccc gga gtt cca ctc ggc acg 1488
156 Ser Leu Ser Gly Arg Phe Tyr Pro Gly Pro Gly Val Pro Leu Gly Thr
157      485      490      495
159 gct atg gtc ttc tcg tac cga gca gct cag gac atg gcg aag taa 1533
160 Ala Met Val Phe Ser Tyr Arg Ala Ala Gln Asp Met Ala Lys
161      500      505      510
163 cgcaattcaa 1543
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167 <211> LENGTH: 510
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169 <213> ORGANISM: Rhodococcus erythropolis
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173 1 5 10 15
175 Gly Gly Ala Leu Thr Gly Ala Tyr Thr Ala Ala Ala Gln Gly Leu Thr
176 20 25 30
178 Thr Ile Val Leu Glu Lys Thr Asp Arg Phe Gly Gly Thr Ser Ala Tyr
179 35 40 45
181 Ser Gly Ala Ser Ile Trp Leu Pro Gly Thr Gln Val Gln Glu Arg Ala
182 50 55 60
184 Gly Leu Pro Asp Ser Thr Glu Asn Ala Arg Thr Tyr Leu Arg Ala Leu
185 65 70 75 80
187 Leu Gly Asp Ala Glu Ser Glu Arg Gln Asp Ala Tyr Val Glu Thr Ala
188 85 90 95
190 Pro Ala Val Val Ala Leu Leu Glu Gln Asn Pro Asn Ile Glu Phe Glu
191 100 105 110
193 Phe Arg Ala Phe Pro Asp Tyr Tyr Lys Ala Glu Gly Arg Met Asp Thr
194 115 120 125
196 Gly Arg Ser Ile Asn Pro Leu Asp Leu Asp Pro Ala Asp Ile Gly Asp

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197      130      135      140
199 Leu Ala Gly Lys Val Arg Pro Glu Leu Asp Gln Asp Arg Thr Gly Gln
200 145      150      155      160
202 Asp His Ala Pro Gly Pro Met Ile Gly Gly Arg Ala Leu Ile Gly Arg
203      165      170      175
205 Leu Leu Ala Ala Val Gln Ser Thr Gly Lys Ala Glu Leu Arg Thr Glu
206      180      185      190
208 Ser Val Leu Thr Ser Leu Ile Val Glu Asp Gly Arg Val Val Gly Ala
209      195      200      205
211 Glu Val Glu Ser Gly Gly Glu Thr Gln Arg Ile Lys Ala Asn Arg Gly
212      210      215      220
214 Val Leu Met Ala Ala Gly Gly Ile Glu Gly Asn Ala Glu Met Arg Glu
215 225      230      235      240
217 Gln Ala Gly Thr Pro Gly Lys Ala Ile Trp Ser Met Gly Pro Phe Gly
218      245      250      255
220 Ala Asn Thr Gly Asp Ala Ile Ser Ala Gly Ile Ala Val Gly Gly Ala
221      260      265      270
223 Thr Ala Leu Leu Asp Gln Ala Trp Phe Cys Pro Gly Val Glu Gln Pro
224      275      280      285
226 Asp Gly Ser Ala Ala Phe Met Val Gly Val Arg Gly Gly Leu Val Val
227      290      295      300
229 Asp Ser Ala Gly Glu Arg Tyr Leu Asn Glu Ser Leu Pro Tyr Asp Gln
230 305      310      315      320
232 Phe Gly Arg Ala Met Asp Ala His Asp Asp Asn Gly Ser Ala Val Pro
233      325      330      335
235 Ser Phe Met Ile Phe Asp Ser Arg Glu Gly Gly Gly Leu Pro Ala Ile
236      340      345      350
238 Cys Ile Pro Asn Thr Ala Pro Ala Lys His Leu Glu Ala Gly Thr Trp
239      355      360      365
241 Val Gly Ala Asp Thr Leu Glu Glu Leu Ala Ala Lys Thr Gly Leu Pro
242      370      375      380
244 Ala Asp Ala Leu Arg Ser Thr Val Glu Lys Phe Asn Asp Ala Ala Lys
245 385      390      395      400
247 Leu Gly Val Asp Glu Glu Phe His Arg Gly Glu Asp Pro Tyr Asp Ala
248      405      410      415
250 Phe Phe Cys Pro Pro Asn Gly Gly Ala Asn Ala Ala Leu Thr Ala Ile
251      420      425      430
253 Glu Asn Gly Pro Phe Tyr Ala Ala Arg Ile Val Leu Ser Asp Leu Gly
254      435      440      445
256 Thr Lys Gly Gly Leu Val Thr Asp Val Asn Gly Arg Val Leu Arg Ala
257      450      455      460
259 Asp Gly Ser Ala Ile Asp Gly Leu Tyr Ala Ala Gly Asn Thr Ser Ala
260 465      470      475      480
262 Ser Leu Ser Gly Arg Phe Tyr Pro Gly Pro Gly Val Pro Leu Gly Thr
263      485      490      495
265 Ala Met Val Phe Ser Tyr Arg Ala Ala Gln Asp Met Ala Lys
266      500      505      510
269 <210> SEQ ID NO: 3
270 <211> LENGTH: 158

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271 <212> TYPE: DNA
272 <213> ORGANISM: Rhodococcus erythropolis
274 <400> SEQUENCE: 3
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277 atctcggcat attgccgct cagtgggacc tggcatggcc ttccagtgcc gtgcggtatt 120
279 ccgtggacac cccaccctct tggagtaagg acgcaatg 158
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283 <211> LENGTH: 19
284 <212> TYPE: DNA
285 <213> ORGANISM: Artificial Sequence
287 <220> FEATURE:
288 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
290 <400> SEQUENCE: 4
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294 <210> SEQ ID NO: 5
295 <211> LENGTH: 624
296 <212> TYPE: DNA
297 <213> ORGANISM: Rhodococcus erythropolis
299 <220> FEATURE:
300 <221> NAME/KEY: CDS
301 <222> LOCATION: (1)..(624)
303 <400> SEQUENCE: 5
304 atg ggg gcg acg ttg ccg aga att gcc gag gtc agg gac gct gct gag 48
305 Met Gly Ala Thr Leu Pro Arg Ile Ala Glu Val Arg Asp Ala Ala Glu
306 1 5 10 15
308 ccc agt tcg gac gag cag cgg gcg cgc cat gtg cgg atg ctg gaa gcg 96
309 Pro Ser Ser Asp Glu Gln Arg Ala Arg His Val Arg Met Leu Glu Ala
310 20 25 30
312 gcc gcc gaa ttg ggg acc gag aaa gaa ctc tca cgg gtt cag atg cac 144
313 Ala Ala Glu Leu Gly Thr Glu Lys Glu Leu Ser Arg Val Gln Met His
314 35 40 45
316 gaa gtt gcc aag cgg gca ggc gtg gcc atc ggc act ctc tac cgc tat 192
317 Glu Val Ala Lys Arg Ala Gly Val Ala Ile Gly Thr Leu Tyr Arg Tyr
318 50 55 60
320 ttc cct tcg aag acg cac ctc ttc gtc gct gtg atg gtc gag cag atc 240
321 Phe Pro Ser Lys Thr His Leu Phe Val Ala Val Met Val Glu Gln Ile
322 65 70 75 80
324 gat cag atc ggc gac agt ttc gcc aag cat cag gtg cag tcg gcc aat 288
325 Asp Gln Ile Gly Asp Ser Phe Ala Lys His Gln Val Gln Ser Ala Asn
326 85 90 95
328 ccg cag gac gcc gtg tac gag gtc ctg gtg cgc gcg act cgc ggg tta 336
329 Pro Gln Asp Ala Val Tyr Glu Val Leu Val Arg Ala Thr Arg Gly Leu
330 100 105 110
332 ctg cgt cgg ccg gcc ctt tcg act gcg atg ctg cag tcg tcc agt acc 384
333 Leu Arg Arg Pro Ala Leu Ser Thr Ala Met Leu Gln Ser Ser Ser Thr
334 115 120 125
336 gcc aac gtc gcg acg gtg ccg gac gtg ggc aag atc gat cgc ggc ttc 432
337 Ala Asn Val Ala Thr Val Pro Asp Val Gly Lys Ile Asp Arg Gly Phe
338 130 135 140

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